

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hall, Frederick L.
Gordon, Erlinda M.
Anderson, W. French
Starnes, Vaughn A.
- (ii) TITLE OF INVENTION: Modified Retroviral Envelope
Polypeptides for Binding to
Extracellular Matrix
Components

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Carella, Byrne, Bain,
Gilfillan, Cecchi, Stewart &
Olstein
- (B) STREET: 6 Becker Farm Road
- (C) CITY: Roseland
- (D) STATE: New Jersey
- (E) COUNTRY: USA
- (F) ZIP: 07068

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch diskette
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: Word Perfect 5.1

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Olstein, Elliot M.

(B) REGISTRATION NUMBER: 24,025

(C) REFERENCE/DOCKET NUMBER: 271010-364

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700

(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(ix) FEATURE:

(A) NAME/KEY: Receptor binding region of ecotropic gp70 protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Ser Pro Gly Ser Ser Pro

5

His Gln Val Tyr Asn Ile Thr Trp Glu Val

10

15

Thr Asn Gly Asp Arg Glu Thr Val Trp Ala

20

25

Thr Ser Gly Asn His Pro Leu Trp Thr Trp

30

35

Trp Pro Asp Leu Thr Pro Asp Leu Cys Met

40

45

Leu Ala His His Gly Pro Ser Tyr Trp Gly

50

55

Leu Glu Tyr Gln Ser Pro Phe Ser Ser Pro

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polynucleotide

(ix) FEATURE:

- (A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCTTCGCCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA	60
GATCGGGAGA CGGTATGGGC AACTTCTGGC AACCACCCTC TGTGGACCTG GTGGCCTGAC	120
CTTACCCAG ATTTATGTAT GTTAGCCAC CATGGACCAT CTTATTGGGG GCTAGAATAT	180
CAATCCCCTT TTTCTTCTCC CCCGGGGCCC CCTTGTTGCT CAGGGGGCAG CAGCCCAGGC	240
TGTTCCAGAG ACTGCGAAGA ACCTTTAACC TCCTCACCC CTCGGTGCAA CACTGCCTGG	300
AACAGACTCA AGCTAGACCA GACAACTCAT AAATCAAATG AGGGATTTTA TGTTTGCCCC	360
GGGCCCCACC GCCCCGAGA ATCCAAGTCA TGTGGGGGTC CAGACTCCTT CTA CTGTGCC	420
TATTGGGGCT GTGAGACAAC CGGTAGAGCT TACTGGAAGC CCTCCTCATC ATGGGATTTC	480
ATCACAGTAA ACAACAATCT CACCTCTGAC CAGGCTGTCC AGGTATGCAA AGATAATAAG	540
TGGTGCAACC CCTTAGTTAT TCGGTTTACA GACGCCGGA GACGGGTTAC TTCCTGGACC	600
ACAGGACATT ACTGGGGCTT ACGTTTGTAT GTCTCCGGAC AAGATCCAGG GCTTACATTT	660
GGGATCCGAC TCAGATACCA AAATCTA	687

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(ix) FEATURE:

- (A) NAME/KEY: collagen-binding domain of von Willebrand Factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Trp Arg Glu Pro Ser Phe Met Ala Leu Ser

5

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